

IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with underlining and deleted text with ~~striketrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

1. (currently amended) A method for predicting a gene expression site, the gene expression site being one of a cell, a tissue and an organ, said method comprising:

calculating a distance between a first gene and each of a plurality of second genes on a genome sequence, where the first gene is an unknown gene having an unknown gene expression site, while the second genes are known genes having known gene expression sites;

extracting the gene expression sites of the second genes from an expression profile database;

determining a first gene expression site, based on the calculated distances ~~distance~~, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, ~~the predetermined distance relation having been determined based on a sensitivity and a specificity that define an upper limit of the distance~~; and

outputting on a display the first gene expression site determined by said determining.

2. (currently amended) The method according to claim 1, wherein each of the calculated distances ~~the distance~~ is smaller than a predetermined threshold.

12 - 24. (cancelled)

25. (currently amended) A computer-readable storage medium encoded with a computer program, including computer executable instructions, for predicting a gene expression site, the gene expression site being one of a cell, a tissue and an organ, and the computer executable instructions, when executed by the computer, cause the computer to perform a method comprising:

calculating a distance between a first gene and each of a plurality of second genes on a genome sequence, where the first gene is an unknown gene having an unknown gene expression site, while the second genes are known genes having known gene expressions sites;

extracting the gene expression sites of the second genes from an expression profile

database;

determining a first gene expression site of the first gene, based on the calculated distances distance, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, ~~the predetermined distance relation having been determined based on a sensitivity and a specificity that define an upper limit of the distance~~; and

outputting on a display the first gene expression site as determined by said determining.

26. (currently amended) The computer program product according to claim 25, wherein each of the calculated distances ~~the distance~~ is smaller than a predetermined threshold.

27. (cancelled)

28. (currently amended) An apparatus for predicting a gene expression site, where the gene expression site is one of a cell, a tissue and an organ, said apparatus comprising:
a calculation unit that calculates a distance between a first gene and each of a plurality of second genes on a genome sequence, where the first gene is an unknown gene having an unknown gene expression site, while the second genes are known genes having known gene expression sites;

an extracting unit that extracts the gene expression sites of the second genes from an expression profile database;

a determination unit that determines a first gene expression site of the first gene, based on the calculated distances distance, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, ~~the predetermined distance relation having been determined based on a sensitivity and a specificity that define an upper limit of the distance~~; and

a display unit that displays the first gene expression site determined by said determination unit.

29. (currently amended) The apparatus according to claim 28, wherein each of the calculated distances ~~the distance~~ is smaller than a predetermined threshold.

30. (cancelled)

31. (previously presented) The method according to claim 1, wherein when the first site and the second site are identical, the second site is deleted from a list before being output.

32. (previously presented) The method according to claim 1,
wherein the sensitivity is a ratio of predicted expression sites for an unknown gene to previously determined expression sites for the unknown gene determined by another method,
and

wherein the specificity is a ratio of unpredicted expression sites for the unknown gene to non-expression sites for the unknown gene previously determined by the other method.

33. (previously presented) A method of determining a gene expression site, comprising:
calculating a distance of an unknown gene having an unknown gene expression site from each of a plurality of known gene expression sites for known genes on a genome sequence
extracting the gene expression sites for known genes from an expression profile database;

outputting on a display a predicted gene expression site of the unknown gene based on a sensitivity, a specificity and the distance calculated between the unknown gene and at least one of the known genes, the distance based on the sensitivity and the specificity which define an upper limit of the distance.

34. (currently amended) The method according to claim 1, wherein the extracting includes weighting each of the gene expression sites based on the calculated distances ~~distance~~ of the corresponding second gene relative to the first gene.

35. (currently amended) The computer-readable medium according to claim 25, wherein the extracting includes weighting each of the gene expression sites based on the calculated distances ~~distance~~ of the corresponding second gene relative to the first gene.

36. (currently amended) The apparatus according to claim 28, wherein the extracting unit weights each of the gene expression sites based on the calculated distances ~~distance~~ of the corresponding second gene relative to the first gene.

37. (new) The method according to claim 1, wherein
the predetermined distance relation is determined based on a sensitivity, indicating a

ratio of expression sites predicted to expression sites previously determined as where the unknown gene expresses by another method, and a specificity, indicating a ratio of expression sites that are predicted to expression sites previously determined as where the unknown gene never expresses by another method, and

a cross-point distance between the specificity and the sensitivity defines an upper limit of the calculated distances.

38. (new) The computer-readable storage medium according to claim 25, wherein the predetermined distance relation is determined based on a sensitivity, indicating a ratio of expression sites predicted to expression sites previously determined as where the unknown gene expresses by another method, and a specificity, indicating a ratio of expression sites that are predicted to expression sites previously determined as where the unknown gene never expresses by another method, and

a cross-point distance between the specificity and the sensitivity defines an upper limit of the calculated distances.

39. (new) The apparatus according to claim 28, wherein the predetermined distance relation is determined based on a sensitivity, indicating a ratio of expression sites predicted to expression sites previously determined as where the unknown gene expresses by another method, and a specificity, indicating a ratio of expression sites that are predicted to expression sites previously determined as where the unknown gene never expresses by another method, and

a cross-point distance between the specificity and the sensitivity defines an upper limit of the calculated distances.

40. (new) A method performed by a processor for predicting a gene expression site, comprising:

calculating distances between a first gene and each of a second gene and a third gene on a genome sequence and having known expression sites;

extracting the expression sites of the second and third genes from a database;

determining a first gene expression site based on the calculated distances as a selected gene expression site of at least one of the second and third genes that has a predetermined distance relation with the first gene that is determined based on a sensitivity, indicating a ratio of expression sites predicted to expression sites previously determined as where the first gene

expresses by another method, and a specificity, indicating a ratio of expression sites that are predicted to expression sites previously determined as where the first gene never expresses by another method, and a cross-point distance between the specificity and the sensitivity defines an upper limit of the calculated distances; and

outputting on a display the determined first gene expression site.